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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/084,139

DATE: 12/26/2002

TIME: 15:11:55

Input Set : A:\2002-12-06 1110-0307P.txt

Output Set: N:\CRF4\12262002\J084139.raw

3 <110> APPLICANT: NAGATA, Shigekazu  
 4 YATOMI, Takehiro  
 5 SUDA, Takashi  
 7 <120> TITLE OF INVENTION: PROPHYLACTIC/THERAPEUTIC AGENT  
 9 <130> FILE REFERENCE: 1110-0307P  
 11 <140> CURRENT APPLICATION NUMBER: 10/084,139  
 C--> 12 <141> CURRENT FILING DATE: 2002-12-09  
 14 <160> NUMBER OF SEQ ID NOS: 12  
 16 <170> SOFTWARE: PatentIn Ver. 2.0  
 18 <210> SEQ ID NO: 1  
 19 <211> LENGTH: 381  
 20 <212> TYPE: DNA  
 21 <213> ORGANISM: Mus sp.  
 23 <220> FEATURE:  
 24 <221> NAME/KEY: CDS  
 25 <222> LOCATION: (1)..(381)  
 27 <400> SEQUENCE: 1  
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 29 Met Met Ser Ser Ala Gln Phe Leu Gly Leu Leu Leu Leu Cys Phe Gln  
 30 1 5 10 15  
 32 ggt acc aga tgt gat atc cag atg aca cag act aca tcc tcc ctg tct 96  
 33 Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser  
 34 20 25 30  
 36 gcc tct ctg gga gac aga gtc acc atc agt tgc agg gcc agt cag gac 144  
 37 Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp  
 38 35 40 45  
 40 att agc aat tat tta aac tgg tat cag cag aaa cca gat gga act gtt 192  
 41 Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val  
 42 50 55 60  
 44 aaa ctc ctg atc tac tac aca tca aga tta cac tca gga gtc cca tca 240  
 45 Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser  
 46 65 70 75 80  
 48 agg ttc agt ggc agt ggg tct ggg aca aat tat tct ctc acc att agc 288  
 49 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asn Tyr Ser Leu Thr Ile Ser  
 50 85 90 95  
 52 aac ctg gaa caa gga gat att gcc act tac ttt tgc caa cag ggt agt 336  
 53 Asn Leu Glu Gln Gly Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Ser  
 54 100 105 110  
 56 acg ctt ccg tgg acg ttc ggt gga ggc acc aag ctg gaa atc aaa 381  
 57 Thr Leu Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
 58 115 120 125  
 61 <210> SEQ ID NO: 2  
 62 <211> LENGTH: 127

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63 <212> TYPE: PRT
64 <213> ORGANISM: Mus sp.
66 <400> SEQUENCE: 2
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68   1             5             10             15
70 Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser
71             20             25             30
73 Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp
74             35             40             45
76 Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val
77             50             55             60
79 Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser
80             65             70             75             80
82 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asn Tyr Ser Leu Thr Ile Ser
83             85             90             95
85 Asn Leu Glu Gln Gly Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Ser
86             100            105            110
88 Thr Leu Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
89             115            120            125
92 <210> SEQ ID NO: 3
93 <211> LENGTH: 408
94 <212> TYPE: DNA
95 <213> ORGANISM: Mus sp.
97 <220> FEATURE:
98 <221> NAME/KEY: CDS
99 <222> LOCATION: (1)..(408)
101 <400> SEQUENCE: 3
102 atg gat tgg gtg tgg acc ttg cta ttc ctg ata gca gct gcc caa agt      48
103 Met Asp Trp Val Trp Thr Leu Leu Phe Leu Ile Ala Ala Ala Gln Ser
104   1             5             10             15
106 gcc caa gca cag atc cag ttg gtg cag tct gga cct gag ctg aag aag      96
107 Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
108             20             25             30
110 cct gga gag aca gtc aag atc tcc tgc aag gct tct ggg tat acc ttc      144
111 Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
112             35             40             45
114 aca gaa tat cca atg cac tgg gtg aag cag gct cca gga aag ggt ttc      192
115 Thr Glu Tyr Pro Met His Trp Val Lys Gln Ala Pro Gly Lys Gly Phe
116             50             55             60
118 aag tgg atg ggc atg ata tac acc gac act gga gag cca tca tat gct      240
119 Lys Trp Met Gly Met Ile Tyr Thr Asp Thr Gly Glu Pro Ser Tyr Ala
120             65             70             75             80
122 gaa gag ttc aag ggg cgg ttt gcc ttc tct ttg gag acc tct gcc agc      288
123 Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
124             85             90             95
126 act gcc tat ttg cag atc aac ttc ctc aaa aat gag gac acg gct aca      336
127 Thr Ala Tyr Leu Gln Ile Asn Phe Leu Lys Asn Glu Asp Thr Ala Thr
128             100            105            110
130 tat ttc tgt gta aga ttt tac tgg gat tac ttt gac tac tgg ggc caa      384

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131 Tyr Phe Cys Val Arg Phe Tyr Trp Asp Tyr Phe Asp Tyr Trp Gly Gln
132          115          120          125
134 ggc acc act ctc aca gtc tcc tca
135 Gly Thr Thr Leu Thr Val Ser Ser
136      130          135
139 <210> SEQ ID NO: 4
140 <211> LENGTH: 136
141 <212> TYPE: PRT
142 <213> ORGANISM: Mus sp.
144 <400> SEQUENCE: 4
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146 1          5          10          15
148 Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
149          20          25          30
151 Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
152          35          40          45
154 Thr Glu Tyr Pro Met His Trp Val Lys Gln Ala Pro Gly Lys Gly Phe
155          50          55          60
157 Lys Trp Met Gly Met Ile Tyr Thr Asp Thr Gly Glu Pro Ser Tyr Ala
158 65          70          75          80
160 Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
161          85          90          95
163 Thr Ala Tyr Leu Gln Ile Asn Phe Leu Lys Asn Glu Asp Thr Ala Thr
164          100          105          110
166 Tyr Phe Cys Val Arg Phe Tyr Trp Asp Tyr Phe Asp Tyr Trp Gly Gln
167          115          120          125
169 Gly Thr Thr Leu Thr Val Ser Ser
170      130          135
173 <210> SEQ ID NO: 5
174 <211> LENGTH: 381
175 <212> TYPE: DNA
176 <213> ORGANISM: Homo sapiens
178 <220> FEATURE:
179 <221> NAME/KEY: CDS
180 <222> LOCATION: (1)..(381)
182 <400> SEQUENCE: 5
183 atg gag acc gat acc ctc ctg cta tgg gtc ctc ctg cta tgg gtc cca
184 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
185 1          5          10          15
187 gga tca acc gga gat att cag atg acc cag agt ccg tcg acc ctc tct
188 Gly Ser Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser
189          20          25          30
191 gct agc gtc ggg gat agg gtc acc ata act tgc agg gca agt cag gac
192 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp
193          35          40          45
195 att tcg aat tat tta aac tgg tat cag cag aag cca ggc aaa gct ccc
196 Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
197          50          55          60
199 aag ctt cta att tat tac aca tca aga tta cac tca ggg gta cct tca

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200 Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser
201 65 70 75 80
203 cgc ttc agt ggc agt gga tct ggg acc aat tat acc ctc aca atc tcg 288
204 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asn Tyr Thr Leu Thr Ile Ser
205 85 90 95
207 agt ctg cag cca gat gat ttc gcc act tat ttt tgc caa cag ggt agt 336
208 Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Ser
209 100 105 110
211 acg ctt ccg tgg acg ttc ggt cag ggg acc aag gtg gag gtc aaa 381
212 Thr Leu Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys
213 115 120 125
216 <210> SEQ ID NO: 6
217 <211> LENGTH: 127
218 <212> TYPE: PRT
219 <213> ORGANISM: Homo sapiens
221 <400> SEQUENCE: 6
222 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
223 1 5 10 15
225 Gly Ser Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser
226 20 25 30
228 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp
229 35 40 45
231 Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
232 50 55 60
234 Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser
235 65 70 75 80
237 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asn Tyr Thr Leu Thr Ile Ser
238 85 90 95
240 Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Ser
241 100 105 110
243 Thr Leu Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys
244 115 120 125
247 <210> SEQ ID NO: 7
248 <211> LENGTH: 408
249 <212> TYPE: DNA
250 <213> ORGANISM: Homo sapiens
252 <220> FEATURE:
253 <221> NAME/KEY: CDS
254 <222> LOCATION: (1)..(408)
256 <400> SEQUENCE: 7
257 atg gat tgg gtg tgg acc ttg cta ttc ctg ata gct gca gcc caa agt 48
258 Met Asp Trp Val Trp Thr Leu Leu Phe Leu Ile Ala Ala Ala Gln Ser
259 1 5 10 15
261 gcc caa gca cag gtc cag ttg gtg cag tct gga gct gag gtg aag aag 96
262 Ala Gln Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
263 20 25 30
265 cct gga agc tca gtc aag gtg tcc tgc aaa gct tct ggg tat acc ttc 144
266 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
267 35 40 45

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269 aca gaa tat cca atg cac tgg gtg aga cag gct cca gga cag ggt ttc 192
270 Thr Glu Tyr Pro Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Phe
271      50                      55                      60
273 aag tgg atg ggc atg ata tac acc gac act gga gag cca tca tat gct 240
274 Lys Trp Met Gly Met Ile Tyr Thr Asp Thr Gly Glu Pro Ser Tyr Ala
275 65                      70                      75                      80
277 gaa gag ttc aag gga cgg ttt aca ttc act ttg gac acc tct acc aac 288
278 Glu Glu Phe Lys Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Asn
279      85                      90                      95
281 act gcc tat atg gag ctc agc tct ctc agg tct gag gac acg gct gtc 336
282 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
283      100                      105                      110
285 tat tac tgt gta aga ttt tac tgg gat tac ttt gac tac tgg ggt caa 384
286 Tyr Tyr Cys Val Arg Phe Tyr Trp Asp Tyr Phe Asp Tyr Trp Gly Gln
287      115                      120                      125
289 ggt acc ctg gtc aca gtc tcc tca 408
290 Gly Thr Leu Val Thr Val Ser Ser
291      130                      135
294 <210> SEQ ID NO: 8
295 <211> LENGTH: 136
296 <212> TYPE: PRT
297 <213> ORGANISM: Homo sapiens
299 <400> SEQUENCE: 8
300 Met Asp Trp Val Trp Thr Leu Leu Phe Leu Ile Ala Ala Ala Gln Ser
301 1                      5                      10                      15
303 Ala Gln Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
304      20                      25                      30
306 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
307      35                      40                      45
309 Thr Glu Tyr Pro Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Phe
310      50                      55                      60
312 Lys Trp Met Gly Met Ile Tyr Thr Asp Thr Gly Glu Pro Ser Tyr Ala
313 65                      70                      75                      80
315 Glu Glu Phe Lys Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Asn
316      85                      90                      95
318 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
319      100                      105                      110
321 Tyr Tyr Cys Val Arg Phe Tyr Trp Asp Tyr Phe Asp Tyr Trp Gly Gln
322      115                      120                      125
324 Gly Thr Leu Val Thr Val Ser Ser
325      130                      135
328 <210> SEQ ID NO: 9
329 <211> LENGTH: 1182
330 <212> TYPE: DNA
331 <213> ORGANISM: Homo sapiens
333 <220> FEATURE:
334 <221> NAME/KEY: CDS
335 <222> LOCATION: (36)..(1169)
337 <400> SEQUENCE: 9

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VERIFICATION SUMMARY

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